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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 8, 2003, 18:16:33 ; Search time 300 Seconds
(without alignments)
8512.554 Million cell updates/sec

Title: US-10-091-628-1
Perfect score: 1134
Sequence: 1 atgagagccaattgttccag.....acatcacttcatgtgaatag 1134

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
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22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	320.4	28.3	2263	16	AAQ91108	Hamster ileal/rena
	2	297.8	26.3	1047	16	AAQ91109	Human ileal/renal
	3	183.2	16.2	1663	24	ABK63719	Rat sequence diffe
	4	173.6	15.3	1580	24	ABN95678	Gene #2176 used to
	5	118.8	10.5	1413	23	AAS64762	DNA encoding novel
	6	86.2	7.6	729	24	AAD33699	Human secreted pro
	7	76.6	6.8	1824	23	AAS64761	DNA encoding novel
	8	67.6	6.0	972	22	AAH67519	C glutamicum codin
c	9	67.6	6.0	349980	22	AAH68532	C glutamicum codin
	10	64.4	5.7	1272	21	AAC39644	Arabidopsis thalia
	11	64.4	5.7	1619	21	AAC49339	Arabidopsis thalia
	12	64.2	5.7	1431	24	ABL39796	Human NS cDNA sequ
c	13	58.2	5.1	269223	22	AAF28554	Genomic fragment #
	14	57.6	5.1	2141	24	AAD22002	Human transporters
	15	53.6	4.7	1005	22	AAH66357	C glutamicum codin
	16	53.6	4.7	1206	21	AAC47338	Arabidopsis thalia
	17	53.6	4.7	1459	21	AAC37731	Arabidopsis thalia
	18	53.6	4.7	349980	22	AAH68528	C glutamicum codin
c	19	46	4.1	30078	21	AAA81520	N. meningitidis pa
c	20	46	4.1	349980	21	AAF21608	Neisseria meningit
c	21	46	4.1	1437668	21	AAA81490	N. meningitidis B
c	22	44.6	3.9	197	22	AAK24436	Human brain expres
c	23	44.6	3.9	600	22	AAK11852	Human brain expres
	24	44.6	3.9	1365	23	ABL15847	Drosophila melanog
c	25	44.6	3.9	2787	23	ABL15846	Drosophila melanog
	26	44	3.9	1431	23	ABL28159	Drosophila melanog
	27	44	3.9	3792	23	ABL28158	Drosophila melanog
	28	43.2	3.8	1425	21	AAA75154	cDNA encoding a mu
	29	43.2	3.8	1425	21	AAA75173	cDNA clone encodin
	30	43.2	3.8	1425	21	AAA75174	cDNA clone encodin
	31	42.6	3.8	912	24	ABK79532	Bacillus clausii g
	32	41.6	3.7	1425	21	AAA75172	cDNA clone encodin
c	33	39	3.4	5403	20	AAV84140	Mouse prothrombina
c	34	38.6	3.4	630	21	AAF08640	Fusarium venenatum
	35	37.8	3.3	65	24	ABN53881	Mouse spliced tran
c	36	37	3.3	249	21	AAC10024	Human secreted pro
c	37	36.8	3.2	3295	24	ABK49478	DNA encoding OSF-2
c	38	36	3.2	396	21	AAH30900	Human colon cancer
c	39	36	3.2	5007	22	AAK52839	Human polynucleoti
c	40	35.8	3.2	2520	23	AAS59595	Propionibacterium
c	41	35.6	3.1	173	21	AAC31209	Human secreted pro
c	42	35.4	3.1	945	23	ABV24385	Human prostate exp
c	43	35.4	3.1	1141	22	AAH57369	Human heart cell s
c	44	35.4	3.1	1149	24	ABN96877	Gene #3375 used to
	45	35	3.1	1749	23	ABL14371	Drosophila melanog

ALIGNMENTS

RESULT 1
AAQ91108
ID AAQ91108 standard; cDNA; 2263 BP.
XX
AC AAQ91108;
XX
DT 17-DEC-1995 (first entry)
XX
DE Hamster ileal/renal bile acid cotransporter.
XX
KW Ileal/renal bile acid cotransporter; therapeutic; gene therapy;
KW diagnostic; ss.
XX
OS Cricetulus griseus.
XX
FH Key Location/Qualifiers
FT CDS 109..1152
FT /*tag= a
XX
PN WO9517905-A1.
XX
PD 06-JUL-1995.
XX
PF 29-DEC-1994; 94WO-US14431.
XX
PR 29-DEC-1993; 93US-0176126.
XX
PA (UYWA-) UNIV WAKE FOREST.
XX
PI Dawson PA;
XX
DR WPI; 1995-246189/32.

DR P-PSDB; AAR77224.
XX
PT Hamster and human ileal and bile acid transport DNA and protein -
PT useful in treatment of e.g. hypercholesterolaemia, diabetes and
PT various digestive diseases, and in gene therapy to restore bile acid
PT uptake activity.
XX
PS Claim 4; Page 98-103; 148pp; English.
XX
CC The ileal/renal bile acid cotransporter cDNA is cloned in an
CC expression vector (plasmid pCMX or plasmid pCMV5) under the control
CC of a baculo virus Autographa californica nuclear-polyhedrosis virus
CC gene promoter, the cytomegalo virus immediate early gene promoter,
CC the SV40 virus late gene promoter or an inducible promoter e.g. the
CC lactose operon promoter, and expressed in CHO, MDCK, CaCo2, BHK or
CC preferably COS-1A cells. The cotransporter is useful in the
CC treatment of hypercholesterolaemia, diabetes, heart disease, liver
CC disease and various digestive disorders. The cDNA may by used in
CC gene therapy to restore bile acid uptake activity to patients whose
CC ileum has been surgically resected for diseases such as Crohn
CC disease, patients born with congenital defects in the bile
CC transporter, and patients suffering from adult-onset chronic
CC idiopathic bile acid diarrhoea. The DNA and protein may be used in
CC screening methods as modulators of ileal/renal bile acid cotransport
CC activity. The DNA can also be used to detect mutations and RFLPs
CC in human ileal/renal bile acid cotransporter genes by amplification
CC with primers (see AAQ91110-15).
XX
SQ Sequence 2263 BP; 672 A; 451 C; 476 G; 664 T; 0 other;

Query Match 28.3%; Score 320.4; DB 16; Length 2263;
Best Local Similarity 60.8%; Pred. No. 5.4e-90;
Matches 522; Conservative 0; Mismatches 336; Indels 0; Gaps 0;

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Qy        80 ATGGAAACCTGGAGCTCGTTTTCACAGTGGTGTCCACTGTGATGATGGGGCTGCTCATGT 139
             | | | |||     | ||  | |     |||  |||  |  |  | |   || | ||||
Db       188 ACGCCATCCTCAGCGTGGTGATGAGCACCGTGCTCACAATCCTCCTAGCCTTGGTGATGT 247

Qy       140 TCTCTTTGGGATGTTCCGTGGAGATCCGGAAGCTGTGGTCGCACATCAGGAGACCCTGGG 199
             | ||  |||| ||    |||||  |||  ||| |    |   ||| | ||| | || ||||
Db       248 TTTCCATGGGGTGCAATGTGGAACTCCACAAGTTTCTGGGACACCTAAGGCGGCCATGGG 307

Qy       200 GCATTGCTGTGGGACTGCTCTGCCAGTTTGGGCTCATGCCTTTTACAGCTTATCTCCTGG 259
             ||||  |  |||||  | ||||| ||||||||  ||||||||  | |||| ||   |||||
Db       308 GCATCGTCGTGGGCTTCCTCTGTCAGTTTGGAATCATGCCTCTCACAGGTTTCGTCCTGT 367

Qy       260 CCATTAGCTTTTCTCTGAAGCCAGTCCAAGCTATTGCTGTTCTCATCATGGGCTGCTGCC 319
             ||  |   ||||     |    ||||| |||||| | |  || || |||  ||| |||||||
Db       368 CCGTGGCCTTTGGCATCCTCCCAGTGCAAGCTGTGGTGGTGCTGATCCAGGGTTGCTGCC 427

Qy       320 CGGGGGGCACCATCTCTAACATTTTCACCTTCTGGGTTGATGGAGATATGGATCTCAGCA 379
             | || || ||   ||| || ||  |  |||  ||||| ||||| || ||||| ||||||
Db       428 CTGGAGGAACTGCCTCCAATATCCTAGCCTATTGGGTAGATGGCGACATGGACCTCAGCG 487

Qy       380 TCAGTATGACAACCTGTTCCACCGTGGCCGCCCTGGGAATGATGCCACTCTGCATTTATC 439
             | || ||||| ||||| |||||  ||   ||||| ||||||||||| || ||| | |
Db       488 TTAGCATGACCACCTGCTCCACGCTGCTTGCCCTTGGAATGATGCCCCTTTGCCTCTTCA 547

Qy       440 TCTACACCTGGTCCTGGAGTCTTCAGCAGAATCTCACCATTCCTTATCAGAACATAGGAA 499
             |||| |||  |   |||  |        ||   |   |||||||| | |  ||| || |
Db       548 TCTATACCAAGATGTGGGTTGACTCAGGGACGATTGTGATTCCTTATGACAGCATTGGCA 607

Qy       500 TTACCCTTGTGTGCCTGACCATTCCTGTGGCCTTTGGTGTCTATGTGAATTACAGATGGC 559
               | | || ||    ||     |||||||  || ||||  | |||||||| ||| |||||
Db       608 CTTCTCTGGTTGCTCTTGTTATTCCTGTTTCCATTGGAATGTATGTGAATCACAAATGGC 667

Qy       560 CAAAACAATCCAAAATCATTCTCAAGATTGGGGCCGTTGTTGGTGGGGTCCTCCTTCTGG 619
             |  || || | || ||||| || || |||||  || | |  ||||   | ||| || |
Db       668 CCCAAAAAGCAAAGATCATACTTAAAATTGGATCCATCGCAGGTGCAATTCTCATTGTTC 727

Qy       620 TGGTCGCAGTTGCTGGTGTGGTCCTGGCGAAAGGATCTTGGAATTCAGACATCACCCTTC 679
             |  |||| || | ||| |   | |||    || |  | ||||     ||   || ||
Db       728 TCATCGCTGTGGTTGGAGGAATACTGTACCAAAGTGCCTGGACCATTGAACCCAAGCTGT 787

Qy       680 TGACCATCAGTTTCATCTTTCCTTTGATTGGCCATGTCACGGGTTTTCTGCTGGCACTTT 739
             ||  ||  |   ||| | |||| |   |||| | | |  ||| ||| | |||||
Db       788 GGATTATAGGAACCATATATCCTATAGCTGGCTACGGCCTGGGGTTTTTCCTGGCTAGAA 847

Qy       740 TTACCCACCAGTCTTGGCAAAGGTGCAGGACAATTTCCTTAGAAACTGGAGCTCAGAATA 799
             ||  |    ||  | ||| | |||||| | ||| || |||| |||| ||    ||||| |
Db       848 TTGCTGGTCAACCCTGGTACAGGTGCCGAACAGTTGCCTTGGAAACCGGGTTGCAGAACA 907

Qy       800 TTCAGATGTGCATCACCATGCTCCAGTTATCTTTCACTGCTGAGCACTTGGTCCAGATGT 859
              |||| ||||   ||||||  | ||| | || ||||   ||||| || |   ||  |||
Db       908 CTCAGCTGTGTTCCACCATTGTGCAGCTTTCCTTCAGCCCTGAGGACCTCAACCTTGTGT 967

Qy       860 TGAGTTTCCCACTGGCCTATGGACTCTTCCAGCTGATAGATGGATTTCTTATTGTTGCAG 919
             | |  ||||| ||   |||  |  |||||||| |       || |    |  | | | ||
Db       968 TCACCTTCCCCCTCATCTACAGCATCTTCCAGATCGCCTTTGCAGCAATACTATTAGGAG 1027

Qy       920 CATATCAGACGTACAAGA 937
             | |||    | |||||||
Db      1028 CTTATGTCGCATACAAGA 1045
```

RESULT 2
AAQ91109
ID AAQ91109 standard; cDNA; 1047 BP.
XX
AC AAQ91109;
XX
DT 17-DEC-1995 (first entry)
XX
DE Human ileal/renal bile acid cotransporter.
XX
KW Ileal/renal bile acid cotransporter; therapeutic; gene therapy;
KW diagnostic; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1044
FT /*tag= a
XX
PN WO9517905-A1.
XX
PD 06-JUL-1995.
XX
PF 29-DEC-1994; 94WO-US14431.
XX
PR 29-DEC-1993; 93US-0176126.
XX
PA (UYWA-) UNIV WAKE FOREST.
XX
PI Dawson PA;
XX
DR WPI; 1995-246189/32.
DR P-PSDB; AAR77225.
XX
PT Hamster and human ileal and bile acid transport DNA and protein -
PT useful in treatment of e.g. hypercholesterolaemia, diabetes and
PT various digestive diseases, and in gene therapy to restore bile acid
PT uptake activity.
XX
PS Claim 5; Page 107-111; 148pp; English.
XX
CC The ileal/renal bile acid cotransporter cDNA is cloned in an
CC expression vector (plasmid pCMX or plasmid pCMV5) under the control
CC of a baculo virus Autographa californica nuclear-polyhedrosis virus
CC gene promoter, the cytomegalo virus immediate early gene promoter,
CC the SV40 virus late gene promoter or an inducible promoter e.g. the
CC lactose operon promoter, and expressed in CHO, MDCK, CaCo2, BHK or
CC preferably COS-1A cells. The cotransporter is useful in the
CC treatment of hypercholesterolaemia, diabetes, heart disease, liver
CC disease and various digestive disorders. The cDNA may by used in
CC gene therapy to restore bile acid uptake activity to patients whose

```
CC   ileum has been surgically resected for diseases such as Crohn
CC   disease, patients born with congenital defects in the bile
CC   transporter, and patients suffering from adult-onset chronic
CC   idiopathic bile acid diarrhoea.  The DNA and protein may be used in
CC   screening methods as modulators of ileal/renal bile acid cotransport
CC   activity.  The DNA can also be used to detect mutations and RFLPs
CC   in human ileal/renal bile acid cotransporter genes by amplification
CC   with primers (see AAQ91110-15).
XX
SQ   Sequence 1047 BP; 251 A; 251 C; 255 G; 290 T; 0 other;

  Query Match             26.3%;  Score 297.8;  DB 16;  Length 1047;
  Best Local Similarity   58.5%;  Pred. No. 4.6e-83;
  Matches  518;  Conservative    0;  Mismatches  367;  Indels    0;  Gaps    0;

Qy         80 ATGGAAACCTGGAGCTCGTTTTCACAGTGGTGTCCACTGTGATGATGGGGCTGCTCATGT 139
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Db         80 ATAACATCCTAAGTGTGGTCCTAAGTACGGTGCTGACCATCCTGTTGGCCTTGGTGATGT 139

Qy        140 TCTCTTTGGGATGTTCCGTGGAGATCCGGAAGCTGTGGTCGCACATCAGGAGACCCTGGG 199
              ||||  |||||||   ||||||  |||  |||  |      ||||||  | | |  || ||||
Db        140 TCTCCATGGGATGCAACGTGGAAATCAAGAAATTTCTAGGGCACATAAAGCGGCCGTGGG 199

Qy        200 GCATTGCTGTGGGACTGCTCTGCCAGTTTGGGCTCATGCCTTTTACAGCTTATCTCCTGG 259
              |||||  |||  ||  | ||||| ||||||||  |||||||  | ||||  |   |||||
Db        200 GCATTTGTGTTGGCTTCCTCTGTCAGTTTGGAATCATGCCCCTCACAGGATTCATCCTGT 259

Qy        260 CCATTAGCTTTTCTCTGAAGCCAGTCCAAGCTATTGCTGTTCTCATCATGGGCTGCTGCC 319
              |  |  ||||     |    ||  |||| ||  |  |  || ||||| || || |||||||
Db        260 CGGTGGCCTTTGACATCCTCCCGCTCCAGGCCGTAGTGGTGCTCATTATAGGATGCTGCC 319

Qy        320 CGGGGGGCACCATCTCTAACATTTTCACCTTCTGGGTTGATGGAGATATGGATCTCAGCA 379
              | || || ||   ||| || || ||  ||| |||| |||| || |||| || |||
Db        320 CTGGAGGAACTGCCTCCAATATCTTGGCCTATTGGGTCGATGGCGACATGGACCTGAGCG 379

Qy        380 TCAGTATGACAACCTGTTCCACCGTGGCCGCCCTGGGAATGATGCCACTCTGCATTTATC 439
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Db        380 TCAGCATGACCACATGCTCCACACTGCTTGCCCTCGGAATGATGCCGCTGTGCCTCCTTA 439

Qy        440 TCTACACCTGGTCCTGGAGTCTTCAGCAGAATCTCACCATTCCTTATCAGAACATAGGAA 499
              ||||  |||      |||             ||   ||   ||||| ||| | |||||||| |
Db        440 TCTATACCAAAATGTGGGTCGACTCTGGGAGCATCGTAATTCCCTATGATAACATAGGTA 499

Qy        500 TTACCCTTGTGTGCCTGACCATTCCTGTGGCCTTTGGTGTCTATGTGAATTACAGATGGC 559
                | || ||     ||    |||||||  || ||||  | | ||| ||| ||| |||||
Db        500 CATCTCTGGTTGCTCTCGTTGTTCCTGTTTCCATTGGAATGTTTGTTAATCACAAATGGC 559

Qy        560 CAAAACAATCCAAAATCATTCTCAAGATTGGGGCCGTTGTTGGTGGGGTCCTCCTTCTGG 619
              |  || || | || ||||| || || |||||| || | |  || |   ||||| || ||
Db        560 CCCAAAAAGCAAAGATCATACTTAAAATTGGGTCCATCGCGGGCGCCATCCTCATTGTGC 619

Qy        620 TGGTCGCAGTTGCTGGTGTGGTCCTGGCGAAAGGATCTTGGAATTCAGACATCACCCTTC 679
              |  | || || | ||| |    |  ||    || |  | ||||      |    ||  ||
Db        620 TCATAGCTGTGGTTGGAGGAATATTGTACCAAAGCGCCTGGATCATTGCTCCCAAACTGT 679

Qy        680 TGACCATCAGTTTCATCTTTCCTTTGATTGGCCATGTCACGGGTTTTCTGCTGGCACTTT 739
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Db        680 GGATTATAGGAACAATATTTCCTGTGGCGGGTTACTCCCTGGGGTTTCTTCTGGCTAGAA 739

Qy        740 TTACCCACCAGTCTTGGCAAAGGTGCAGGACAATTTCCTTAGAAACTGGAGCTCAGAATA 799
              || |    |   | ||| | |||||| | ||  ||  | || ||||| ||    |||||
Db        740 TTGCTGGTCTACCCTGGTACAGGTGCCGAACGGTTGCTTTTGAAACGGGGATGCAGAACA 799

Qy        800 TTCAGATGTGCATCACCATGCTCCAGTTATCTTTCACTGCTGAGCACTTGGTCCAGATGT 859
              |||  | ||   ||||||  | ||| | || |||||| |||||  |  |         | |
Db        800 CGCAGCTATGTTCCACCATCGTTCAGCTCTCCTTCACTCCTGAGGAGCTCAATGTCGTAT 859

Qy        860 TGAGTTTCCCACTGGCCTATGGACTCTTCCAGCTGATAGATGGATTTCTTATTGTTGCAG 919
              | |  ||||| ||   |||  |  | ||||||||      ||      |  |  | | |
Db        860 TCACCTTCCCGCTCATCTACAGCATTTTCCAGCTCGCCTTTGCCGCAATATTCTTAGGAT 919

Qy        920 CATATCAGACGTACAAGAGGAGATTGAAGAACAAACATGGAAAAA 964
                |||  | | |||||||   |       || ||  | | | |||
Db        920 TTTATGTGGCATACAAGAAATGTCATGGAAAAAACAAGGCAGAAA 964


RESULT 3
ABK63719
ID   ABK63719 standard; cDNA; 1663 BP.
XX
AC   ABK63719;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Rat sequence differentially expressed in response to a hepatotoxin #1626.
XX
KW   Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;
KW   differential expression; centrilobular necrosis; steatosis.
XX
OS   Rattus norvegicus.
XX
PN   WO200210453-A2.
XX
PD   07-FEB-2002.
XX
PF   30-JUL-2001; 2001WO-US23872.
XX
PR   31-JUL-2000; 2000US-222040P.
PR   02-NOV-2000; 2000US-244880P.
PR   11-MAY-2001; 2001US-290029P.
PR   15-MAY-2001; 2001US-290645P.
PR   22-MAY-2001; 2001US-292336P.
PR   06-JUN-2001; 2001US-295798P.
PR   13-JUN-2001; 2001US-297457P.
PR   19-JUN-2001; 2001US-298884P.
PR   09-JUL-2001; 2001US-303459P.
XX
PA   (GENE-) GENE LOGIC INC.
XX
PI   Mendrick D,  Porter MW,  Johnson KR,  Castle AL,  Elashoff MR;
XX
DR   WPI; 2002-241625/29.
XX
PT   Predicting toxic effects of compounds or the progression of these toxic
PT   effects by determining the changes in gene expression in tissues or
PT   cells exposed to the toxin and comparing these to gene expression in
PT   unexposed tissues or cells -
XX
PS   Claim 1; Seq ID No 1626; 239pp; English.
XX
CC   The invention relates to methods for predicting toxic effects of
CC   compounds or the progression of these toxic effects by determining the
CC   global changes in gene expression in tissues or cells exposed to the
CC   toxin and comparing these to gene expression in unexposed tissues or
CC   cells. Also included are methods of predicting at least one toxic
CC   effect of a compound or progression of a toxic effect, preferably the
CC   hepatotoxicity of a compound, comprising detecting the level of
CC   expression in a tissue or cell sample exposed to the compound of two or
CC   more genes listed in the specification, where  differential expression of
CC   the genes is indicative of at least one toxic effect or progression.
CC   The method can also be used to identify an agent which modulates the
CC   toxic response and predict cellular pathways that a compound modulates
CC   in a cell. The methods utilise a set of at least two probes (on a solid
CC   support in kit form), where each of the probes comprises a sequence that
CC   specifically hybridises to a gene listed in the specification, a computer
CC   system comprising a database containing information identifying the
CC   expression level in a tissue or cell sample exposed to a hepatotoxin of a
CC   set of genes comprising at least two genes listed in the specification,
CC   and a user interface to view the information used to present information
CC   identifying the expression level in a tissue or cell of at least one gene
CC   listed in the specification. The method is useful for elucidating global
CC   changes in gene expression and for identifying toxicity markers in
CC   tissues or cell exposed to a known toxin. The genes may be used as
CC   toxicity markers in drug screening and toxicity assays. The genes and
CC   gene expression information may be used as diagnostic markers for the
CC   prediction or identification of the physiological state of tissue or cell
```

CC sample that has been exposed to a compound or agent. Hepatotoxicity
CC is characterised by centrilobular necrosis and steatosis. The present
CC sequence is an expressed sequence tag (EST) or cDNA derived from a gene
CC which is differentially expressed in response to a hepatotoxic agent.
XX
SQ Sequence 1663 BP; 450 A; 460 C; 325 G; 428 T; 0 other;

Query Match 16.2%; Score 183.2; DB 24; Length 1663;
Best Local Similarity 53.6%; Pred. No. 8.9e-47;
Matches 430; Conservative 0; Mismatches 363; Indels 9; Gaps 2;

Qy 119 TGATGATGGGGCTGCTCATGTTCTCTTTGGGATGTTCCGTGGAGATCCGGAAGCTGTGGT 178
Db 219 TAATGTTGCTGCTTATCATGCTCTCACTGGGCTGCACCATGGAATTCAGCAAGATCAAGG 278

Qy 179 CGCACATCAGGAGACCCTGGGGCATTGCTGTGGGACTGCTCTGCCAGTTTGGGCTCATGC 238
Db 279 CTCACTTGTGGAAGCCCAAAGGGGTGATCGTTGCCTTGGTGGCCCAGTTTGGCATCATGC 338

Qy 239 CTTTTACAGCTTATCTCCTGGCCATTAGCTTTTCTCTGAAGCCAGTCCAAGCTATTGCTG 298
Db 339 CCCTCGCTGCTTTTCTTCTCGGCAAGATCTTTCACCTGAGCAACATTGAAGCTCTGGCCA 398

Qy 299 TTCTCATCATGGGCTGCTGCCCGGGGGGCACCATCTCTAACATTTTCACCTTCTGGGTTG 358
Db 399 TCCTCATCTGTGGCTGCTCTCCCGGGGGGAACTTGTCCAACCTCTTCACCCTGGCCATGA 458

Qy 359 ATGGAGATATGGATCTCAGCATCAGTATGACAACCTGTTCCACCGTGGCCGCCCTGGGAA 418
Db 459 AGGGGGACATGAACCTCAGCATCGTGATGACCACCTGCTCCAGCTTCAGTGCCTTGGGCA 518

Qy 419 TGATGCCACTCTGCATTTATCTCTACACC---TGGTCCTGGAGTCTTCAGCAGAATCTCA 475
Db 519 TGATGCCACTCCTCTTATACGTCTACAGCAAAGGCATCTACGATGGAGACCTTAAGGACA 578

Qy 476 CCATTCCTTATCAGAACATAGGAATTACCCTTGTGTGCCTGACCATTCCTGTGGCCTTTG 535
Db 579 AGGTGCCCTACAAAGGCATTATGATATCACTAGTCATAGTTCTCATTCCTTGCACCATAG 638

Qy 536 GTGTCTATGTGAATTACAGATGGCCAAAACAATCCAAAATCATTCTCAAGATTGGGGCCG 595
Db 639 GGATCGTCCTCAAGTCCAAAAGGCCACACTATGTACCCTACATCCTCAAGGGAGGCATGA 698

Qy 596 TTGTTGGTGGGGTCCTCCTTCTGGTGGTCGCAGTTGCTGGTGTGGTCCTGGCGAAAGGAT 655
Db 699 TCATCACCTTCCTCCTCTCTGTGGCTGTCACAGCCCTCTCTGTCATCAATGTGGGCAACA 758

Qy 656 CTTGGAATTCAGACATCAC------CCTTCTGACCATCAGTTTCATCTTTCCTTTGATTG 709
Db 759 GCATCATGTTCGTCATGACACCACACTTACTGGCTACCTCCTCCCTGATGCCCTTCTCTG 818

Qy 710 GCCATGTCACGGGTTTTCTGCTGGCACTTTTTACCCACCAGTCTTGGCAAAGGTGCAGGA 769
Db 819 GCTTTCTGATGGGTTACATTCTCTCTGCTCTCTTCCAACTCAATCCAAGCTGCAGACGCA 878

Qy 770 CAATTTCCTTAGAAACTGGAGCTCAGAATATTCAGATGTGCATCACCATGCTCCAGTTAT 829
Db 879 CCATCAGCATGGAAACAGGATTCCAAAACATTCAACTCTGTTCTACCATCCTCAATGTGA 938

Qy 830 CTTTCACTGCTGAGCACTTGGTCCAGATGTTGAGTTTCCCACTGGCCTATGGACTCTTCC 889
Db 939 CCTTCCCCCCTGAAGTCATTGGGCCACTTTTCTTCTTTCCTCTCCTCTACATGATTTTCC 998

Qy 890 AGCTGATAGATGGATTTCTTAT 911
Db 999 AGCTTGCAGAAGGACTTCTCAT 1020

RESULT 4
ABN95678
ID ABN95678 standard; DNA; 1580 BP.
XX
AC ABN95678;
XX
DT 13-AUG-2002 (first entry)
XX
DE Gene #2176 used to diagnose liver cancer.
XX
KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
KW metastatic liver tumour; cytostatic; expression profile; disease state;
KW disease progression; drug toxicity; drug efficacy; drug metabolism.
XX
OS Homo sapiens.
XX
PN WO200229103-A2.
XX
PD 11-APR-2002.
XX
PF 02-OCT-2001; 2001WO-US30589.
XX
PR 02-OCT-2000; 2000US-237054P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
XX
DR WPI; 2002-426119/45.
XX
PT Diagnosing and detecting the progression of liver cancer,
PT hepatocellular carcinoma or metastatic liver tumor in a patient,
PT involves detecting the level of expression of two or more genes in a
PT liver tissue sample -
XX
PS Claim 1; SEQ ID NO 2176; 298pp; English.
XX
CC The invention relates to a novel method for diagnosing and detecting the
CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC tumour in a patient, and differentiating metastatic liver cancer from
CC hepatocellular carcinoma in a patient, involving detecting the level of
CC expression of two or more genes represented in ABN93503-ABN97455 in a
CC tissue sample. The method of the invention has hepatotropic, and
CC cytostatic activity. The method is useful for diagnosing and detecting
CC the progression of liver cancer, hepatocellular carcinoma and metastatic
CC liver carcinoma in a patient. The method is useful for identifying
CC expression profiles which serve as useful diagnostic markers as well as
CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1580 BP; 400 A; 434 C; 341 G; 405 T; 0 other;

Query Match 15.3%; Score 173.6; DB 24; Length 1580;
Best Local Similarity 51.9%; Pred. No. 9.2e-44;
Matches 445; Conservative 0; Mismatches 404; Indels 9; Gaps 2;

Qy 119 TGATGATGGGGCTGCTCATGTTCTCTTTGGGATGTTCCGTGGAGATCCGGAAGCTGTGGT 178
Db 180 TCATGTTGTTCTTCATCATGCTCTCGCTGGGCTGCACCATGGAGTTCAGCAAGATCAAGG 239

Qy 179 CGCACATCAGGAGACCCTGGGGCATTGCTGTGGGACTGCTCTGCCAGTTTGGGCTCATGC 238
Db 240 CTCACTTATGGAAGCCTAAAGGGCTGGCCATCGCCCTGGTGGCACAGTATGGCATCATGC 299

Qy 239 CTTTTACAGCTTATCTCCTGGCCATTAGCTTTTCTCTGAAGCCAGTCCAAGCTATTGCTG 298
Db 300 CCCTCACGGCCTTTGTGCTGGGCAAGGTCTTCCGGCTGAAGAACATTGAGGCACTGGCCA 359

Qy 299 TTCTCATCATGGGCTGCTGCCCGGGGGGCACCATCTCTAACATTTTCACCTTCTGGGTTG 358
Db 360 TCTTGGTCTGTGGCTGCTCACCTGGAGGGAACCTGTCCAATGTCTTCAGTCTGGCCATGA 419

Qy 359 ATGGAGATATGGATCTCAGCATCAGTATGACAACCTGTTCCACCGTGGCCGCCCTGGGAA 418
Db 420 AGGGGGACATGAACCTCAGCATTGTGATGACCACCTGCTCCACCTTCTGTGCCCTTGGCA 479

```
Qy        419 TGATGCCACTCTGCATTTATCTCTACACC---TGGTCCTGGAGTCTTCAGCAGAATCTCA 475
              ||||||| |||  | | ||  ||||| ||    ||  ||     |    | | |||   ||
Db        480 TGATGCCTCTCCTCCTGTACATCTACTCCAGGGGGATCTATGATGGGGACCTGAAGGACA 539

Qy        476 CCATTCCTTATCAGAACATAGGAATTACCCTTGTGTGCCTGACCATTCCTGTGGCCTTTG 535
              | || ||| |   ||| |  ||  | || ||      |   |||||||    || | |
Db        540 AGGTGCCCTATAAAGGCATCGTGATATCACTGGTCCTGGTTCTCATTCCTTGCACCATAG 599

Qy        536 GTGTCTATGTGAATTACAGATGGCCAAAACAATCCAAAATCATTCTCAAGATTGGGGCCG 595
              |  ||     | || | || | |||||  || |            |  |||||   |||
Db        600 GGATCGTCCTCAAATCCAAACGGCCACAATACATGCGCTATGTCATCAAGGGAGGGATGA 659

Qy        596 TTGTTGGTGGGGTCCTCCTTCTGGTGGTCGCAGTTGCTGGTGTGGTCCTGGCGAAAGGAT 655
              |  |   |    |   | | |||  ||| |||||     ||   ||   | |
Db        660 TCATCATTCTCTTGTGCAGTGTGGCCGTCACAGTTCTCTCTGCCATCAATGTGGGGAAGA 719

Qy        656 CTTGGAATTCAGACATCAC------CCTTCTGACCATCAGTTTCATCTTTCCTTTGATTG 709
                |  | | ||| ||       | |  |  ||| |   | | |  | ||||| ||||
Db        720 GCATCATGTTTGCCATGACACCACTCTTGATTGCCACCTCCTCCCTGATGCCTTTTATTG 779

Qy        710 GCCATGTCACGGGTTTTCTGCTGGCACTTTTTACCCACCAGTCTTGGCAAAGGTGCAGGA 769
              ||  | |   ||||| | | ||  |   | |   |  ||    | | |   | |  | |
Db        780 GCTTTCTGCTGGGTTATGTTCTCTCTGCTCTCTTCTGCCTCAATGGACGGTGCAGACGCA 839

Qy        770 CAATTTCCTTAGAAACTGGAGCTCAGAATATTCAGATGTGCATCACCATGCTCCAGTTAT 829
              |  |   | | || ||||||   || ||| | ||  | ||   ||||||  ||| |  |
Db        840 CTGTCAGCATGGAGACTGGATGCCAAAATGTCCAACTCTGTTCCACCATCCTCAATGTGG 899

Qy        830 CTTTCACTGCTGAGCACTTGGTCCAGATGTTGAGTTTCCCACTGGCCTATGGACTCTTCC 889
              | ||  |  ||||   | | |  |   | ||    || || ||   |||     | ||||
Db        900 CCTTTCCACCTGAAGTCATTGGACCACTTTTCTTCTTTCCCCTCCTCTACATGATTTTCC 959

Qy        890 AGCTGATAGATGGATTTCTTATTGTTGCAGCATATCAGACGTACAAGAGGAGATTGAAGA 949
              ||||   ||| ||  |||   |  ||||   || |  |   ||  |||      ||
Db        960 AGCTTGGAGAAGGGCTTCTCCTCATTGCCATATTTTGGTGCTATGAGAAATTCAAGACTC 1019

Qy        950 ACAAACATGGAAAAAAGA 967
              |||  ||  || ||| |
Db       1020 CCAAGGATAAAACAAAAA 1037
```

RESULT 5
AAS64762
ID AAS64762 standard; cDNA; 1413 BP.
XX
AAS64762;

13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #566.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG00575.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 566; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1413 BP; 374 A; 334 C; 345 G; 360 T; 0 other;

Query Match 10.5%; Score 118.8; DB 23; Length 1413;
Best Local Similarity 62.4%; Pred. No. 1.7e-26;
Matches 186; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

```
Qy         80 ATGGAAACCTGGAGCTCGTTTTCACAGTGGTGTCCACTGTGATGATGGGGCTGCTCATGT 139
              ||   | |||     | ||  | |    ||||   ||  |  || |||   || | ||||
Db        863 ATAACATCCTAAGTGTGGTCCTAAGTACGGTGCTGACCATCCTGTTGGCCTTGGTGATGT 922

Qy        140 TCTCTTTGGGATGTTCCGTGGAGATCCGGAAGCTGTGGTCGCACATCAGGAGACCCTGGG 199
              ||||  |||||||   ||||| |||  |||  |      |||||| | | | || ||||
Db        923 TCTCCATGGGATGCAACGTGGAAATCAAGAAATTTCTAGGGCACATAAAGCGGCCGTGGG 982

Qy        200 GCATTGCTGTGGGACTGCTCTGCCAGTTTGGGCTCATGCCTTTTACAGCTTATCTCCTGG 259
              |||||  ||| ||  | ||||| ||||||||  |||||||  | ||||  |   |||||
Db        983 GCATTTGTGTTGGCTTCCTCTGTCAGTTTGGAATCATGCCCCTCACAGGATTCATCCTGT 1042

Qy        260 CCATTAGCTTTTCTCTGAAGCCAGTCCAAGCTATTGCTGTTCTCATCATGGGCTGCTGCC 319
              |  |   ||||   |    ||  |||| ||  | |  || ||||| || || |||||||
Db       1043 CGGTGGCCTTTGACATCCTCCCGCTCCAGGCCGTAGTGGTGCTCATTATAGGATGCTGCC 1102

Qy        320 CGGGGGGCACCATCTCTAACATTTTCACCTTCTGGGTTGATGGAGATATGGATCTCAG 377
              | || || ||   ||| || || ||  |||  ||||| |||| || ||||| || ||
Db       1103 CTGGAGGAACTGCCTCCAATATCTTGGCCTATTGGGTCGATGGCGACATGGACCTGAG 1160
```

RESULT 6
AAD33699
ID AAD33699 standard; cDNA; 729 BP.
XX
AC AAD33699;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human secreted protein-encoding gene 8 cDNA clone HBCPB32, SEQ ID NO:18.
XX
KW Human; secreted protein; immune disorder; antiallergic; antirheumatic;
KW rheumatoid arthritis; breast neoplasia; breast cancer; antiarthritic;
KW neurological disease; Alzheimer's disease; Parkinson's disease; trauma;
KW Tourette syndrome; encephalitis; cytostatic; haemostatic; anaemia; mania;
KW antiinflammatory; ophthalmalogical; dermatological; immunostimulatory;
KW immunomodulatory; immunosuppressive; antibacterial; antipsoriatic;
KW gene therapy; autoimmune disease; Huntington's disease; meningitis;

```
KW   demyelinating disease; peripheral neuropathy; congenital malformation;
KW   spinal cord injury; peripheral neuropathy; ischaemia; perception;
KW   multiple sclerosis; infarction; haemorrhage; schizophrenia; dementia;
KW   depression; panic disorder; learning disability; ALS; feeding disorder;
KW   hyperproliferative disorder; sleep pattern; cardiovascular disorder;
KW   reproductive disorder; digestive system disorder; behavioural disorder;
KW   gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             89..679
FT                   /*tag=  a
FT                   /product= "Human secreted protein"
FT                   /transl_except= (pos:599..601, aa:Xaa)
FT                   /transl_except= (pos:611..613, aa:Xaa)
FT                   /transl_except= (pos:617..619, aa:Xaa)
FT                   /transl_except= (pos:629..631, aa:Xaa)
FT                   /transl_except= (pos:641..643, aa:Xaa)
FT                   /transl_except= (pos:650..652, aa:Xaa)
FT                   /transl_except= (pos:653..655, aa:Xaa)
FT                   /note= "Xaa equals any of the naturally occurring
FT                   L-amino acids"
FT   sig_peptide     89..199
FT                   /*tag=  b
FT   mat_peptide     200..676
FT                   /*tag=  c
FT                   /product= "Human mature secreted protein"
XX
PN   WO200216390-A1.
XX
PD   28-FEB-2002.
XX
PF   17-JAN-2001; 2001WO-US01435.
XX
PR   18-AUG-2000; 2000US-226282P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Komatsoulis GA,  Baker KP,  Birse CE,  Soppet DR,  Olsen HS;
PI   Moore PA,  Wei P,  Ebner R,  Duan DR,  Shi Y,  Choi GH,  Fiscella M;
PI   Ni J;
XX
DR   WPI; 2002-304113/34.
DR   P-PSDB; AAE21198.
XX
PT   An isolated nucleic acid molecule (I) comprising a polynucleotide which
PT   encodes a polypeptide useful in the diagnosis and treatment of
PT   disorders e.g. immune disorders -
XX
PS   Claim 1; Page 445; 534pp; English.
XX
CC   AAD33692-AAD33736 represent cDNAs corresponding to 21 human secreted
CC   protein genes, and AAE21191-AAE21235 represent the proteins they encode.
CC   AAE21236-AAE21280 represent human secreted protein fragments. The genes
CC   and their corresponding secreted proteins are useful for preventing,
CC   treating or ameliorating medical conditions, e.g., by protein or gene
CC   therapy. Pathological conditions can be diagnosed by determining the
CC   amount of the new protein in a sample or by determining the presence of
CC   mutations in the new genes. Specific uses are described for each of the
CC   21 genes, based on the tissues in which they are most highly expressed,
CC   and include developing products for the diagnosis or treatment of
CC   immune or autoimmune diseases e.g. AIDS (acquired immune deficiency
CC   syndrome), asthma, anaemia and rheumatoid arthritis, breast neoplasia
CC   and breast cancer, neurological diseases e.g. Alzheimer's disease,
CC   Parkinson's disease, Huntington's disease, Tourette syndrome,
CC   meningitis, demyelinating disease, peripheral neuropathies, neoplasia,
CC   trauma, congenital malformations, spinal cord injuries, toxic
CC   neuropathies induced by neurotoxins, peripheral neuropathies, multiple
CC   sclerosis, ischaemia and infarction, haemorrhages, schizophrenia, mania,
CC   dementia, depression, panic disorder, learning disabilities, ALS,
CC   altered behaviours e.g. disorders in feeding, sleep patterns, balance
CC   and perception, encephalitis, disorders in cardiovascular, neural/
CC   sensory, reproductive and digestive systems, behavioural disorders and
CC   hyperproliferative disorder. The present sequence represents a human
CC   secreted protein-encoding cDNA of the invention.
XX
SQ   Sequence 729 BP; 148 A; 190 C; 169 G; 210 T; 12 other;

  Query Match             7.6%;  Score 86.2;  DB 24;  Length 729;
  Best Local Similarity   49.0%;  Pred. No. 2.2e-16;
  Matches  352;  Conservative    9;  Mismatches  339;  Indels   19;  Gaps    5;

Qy        256 CTGGCCATTAGCTTTTCTCTGAAGCCAGTCCAAGCTATTGCTGTTCTCATCATGGGCTGC 315
              |||||| |   |||     ||| |     ||     ||  | || || ||| |    ||||||
Db          2 CTGGCCCTCGCCTTCAAGCTGGACGAGGTGGCCGCCGTGGCGGTGCTCCTGTGTGGCTGC 61

Qy        316 TGCCCGGGGGGCACCATCTCTAACATTTTCACCTTCTGGGTTGATGGAGATATGGATCTC 375
              || || || ||||   |||| ||  || |  || |   |||||| || || ||| | |||
Db         62 TGTCCCGGCGGCAATCTCTCCAATCTTATGTCCCTGCTGGTTGACGGCGACATGAACCTC 121

Qy        376 AGCATCAGTATGACAACCTGTTCCACCGTGGCCGCCCTGGGAATGATGCCACTCTGCATT 435
              |||||||  ||||| | ||  |||||  |    |||||  |   |||||| || ||| |
Db        122 AGCATCATCATGACCATCTCCTCCACGCTTCTGGCCCTCGTCTTGATGCCCCTGTGCCTG 181

Qy        436 TATCTCTACACCTGGTCCTGGAGTCTTCAGCAGAATCTCACCATTCCTTATC----AGAA 491
              |   |||||| |||| | |||| ||  || |  |||   |  || ||   |      ||
Db        182 TGGATCTACAGCTGGGCTTGGA-TCAACACCCCTATCGTGCAGTTACTACCCCTAGGGAC 240

Qy        492 CATAGGAATTACCCTTGTGTGCCTGACCATTCCTGTGGCCTTTGGTGTCTATGTGAATTA 551
              | |     | || ||      ||      ||| ||| | |  || || ||||   |    ||
Db        241 CGTGACCCTGACTCTCTGCAGCACTCTCATACCTATCGGGTTGGGCGTCTTCATTCGCTA 300

Qy        552 CAGATGGCCAAAACAATCCAAAATCATTCTCAAGATTGGGGCCGTTGTTGGTGGGGTCCT 611
              || ||          |  |  |||| | ||| ||    || |       |  | | |
Db        301 CAAATACAGCCGGGTGGCTGACTACATTGTGAAGGTT---TCCCTGTGGTCTCTGCTAGT 357

Qy        612 CCTTCTGGTGGTCGCAGTTGCTGGTGTGGTCCTGGCGAAAGGATCTTGGAATTCAGACAT 671
                |||||||||||     |          | |      |  |||| ||          |  |
Db        358 GACTCTGGTGGTCCTTTTCATAATGACCGGCACTATGTTAGGACCTGAACTGCTGGCAAG 417

Qy        672 CACCCTTCTGACCATCAGTTTCA---------TCTTTCCTTTGATTGGCCATGTCACGGG 722
              | || |    |  |  | | |          |  | ||||||   ||| | |   | ||
Db        418 TATCCCTGCAGCTGTTTATGTGATAGCAATTTTTATGCCTTTGGCAGGCTACGCTTCAGG 477

Qy        723 TTTTCTGCTGGCACTTTTTACCCACCAGTCTTGGCAAAGGTGCAGGACAATTTCCTTAGA 782
              || |    | ||   | |  |||  |    |  |    |||||  | |   | ||
Db        478 TTATGGTTTAGCTACTCTCTTCCATCTTCCACCCAACTGCAAGAGGACTGTATGTCTGGA 537

Qy        783 AACTGGAGCTCAGAATATTCAGATGTGCATCACCATGCTCCAGTTATCTTTCACTGCTGA 842
              |||  ||   |||||| | ||| | ||  |    |||| ||  |  |  | ||    | ||
Db        538 AACAGGTAGTCAGAATGTGCAGCTCTGTACAGCCATTCTAAAACTGGCCTT--TCACCGA 595

Qy        843 GCACTTGGTCCAGATGTTGAGTTTCCCACTGGCCTATGGACTCTTCCAGCTGATAGATGG 902
                : | |      |||:  |  :| ||  ||   :||| ||| ||:|||     |:| :
Db        596 ATTYATAGGAAGCATGKACATGKTTCCTTTGCTGKATGCACTTTTYCAGTCTGCARAASC 655

Qy        903 ATTTCTTATTGTTGCAGCATATCAGACGTACAAGAGGAGATTGAAGAACAAACATGGAA 961
                  || |||:|  |   ||| | | |||    |:   | ||  | || ||    |||
Db        656 GGGGATTTTTGKTTTAATCTATAAAAKGTATGGAARTGAAATGTTGNACCAAGCNAGAA 714


RESULT 7
AAS64761
ID   AAS64761 standard; cDNA; 1824 BP.
XX
AC   AAS64761;
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #565.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
```

XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG00574.
XX
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 565; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1824 BP; 409 A; 477 C; 486 G; 452 T; 0 other;

Query Match 6.8%; Score 76.6; DB 23; Length 1824;
Best Local Similarity 58.6%; Pred. No. 4.1e-13;
Matches 133; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

```
Qy        80 ATGGAAACCTGGAGCTCGTTTTCACAGTGGTGTCCACTGTGATGATGGGGCTGCTCATGT 139
             ||   | |||     | ||  | |    ||||   ||  |  || |||   || | ||||
Db        80 ATAACATCCTAAGTGTGGTCCTAAGTACGGTGCTGACCATCCTGTTGGCCTTGGTGATGT 139

Qy       140 TCTCTTTGGGATGTTCCGTGGAGATCCGGAAGCTGTGGTCGCACATCAGGAGACCCTGGG 199
             ||||  |||||||   ||||||  |||  |||  |      ||||||  | | | || ||||
Db       140 TCTCCATGGGATGCAACGTGGAAATCAAGAAATTTCTAGGGCACATAAAGCGGCCGTGGG 199

Qy       200 GCATTGCTGTGGGACTGCTCTGCCAGTTTGGGCTCATGCCTTTTACAGCTTATCTCCTGG 259
             |||||  |||  ||  | |||||  ||||||||  |||||||  | ||||  |   |||||
Db       200 GCATTTGTGTTGGCTTCCTCTGTCAGTTTGGAATCATGCCCCTCACAGGATTCATCCTGT 259

Qy       260 CCATTAGCTTTTCTCTGAAGCCAGTCCAAGCTATTGCTGTTCTCATC 306
             |  |   ||||    |    ||  |||| ||  | |      || |||
Db       260 CGGTGGCCTTTGACATCCTCCCGCTCCAGGCCGTAGTGAAACTTATC 306
```

RESULT 8
AAH67519
ID AAH67519 standard; DNA; 972 BP.
XX
AC AAH67519;
XX
DT 26-SEP-2001 (first entry)
XX
DE C glutamicum coding sequence fragment SEQ ID NO: 2554.
XX
KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KW organic acid synthesis; ds.
XX
OS Corynebacterium glutamicum.
XX
PN EP1108790-A2.
XX
PD 20-JUN-2001.
XX
PF 18-DEC-2000; 2000EP-0127688.
XX
PR 16-DEC-1999; 99JP-0377484.
PR 07-APR-2000; 2000JP-0159162.
PR 03-AUG-2000; 2000JP-0280988.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
DR WPI; 2001-376931/40.
DR P-PSDB; AAG92300.
XX
PT Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analysing
PT expression profile or pattern of a gene and identifying homologous gene
PT -
XX
PS Claim 8; SEQ ID NO: 2554; 246pp + Sequence Listing; English.
XX
CC The present invention provides a number of nucleotide and protein
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of coryneform bacterium, measuring expression amount and
CC analysing the expression profile or expression pattern of a gene derived
CC from Coryneform bacterium, and identifying a homologue of a gene derived
CC from coryneform bacterium. Coryneform bacteria are useful for producing
CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC European Patent Office.
XX
SQ Sequence 972 BP; 198 A; 274 C; 241 G; 259 T; 0 other;

Query Match 6.0%; Score 67.6; DB 22; Length 972;
Best Local Similarity 51.3%; Pred. No. 2e-10;
Matches 157; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

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Qy       129 GCTGCTCATGTTCTCTTTGGGATGTTCCGTGGAGATCCGGAAGCTGTGGTCGCACATCAG 188
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Db       141 GATCATCATGTTCACCATGGGTTTGACCTTGACGGTGCCCGATTTTCAGATGGTGCTTAA 200

Qy       189 GAGACCCTGGGGCATTGCTGTGGGACTGCTCTGCCAGTTTGGGCTCATGCCTTTTACAGC 248
             | ||   |   ||      | ||  |  |    |||||||   |||||||  ||    ||
Db       201 ACGTCCACTGCCTATCTTGATCGGTGTAGTAGCGCAGTTTGTCATCATGCCATTCCTGGC 260

Qy       249 TTATCTCCTGGCCATTAGCTTTTCTCTGAAGCCAGTCCAAGCTATTGCTGTTCTCATCAT 308
                 | || |  |  ||     || || ||||  |  ||  |||   |||||||  |
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Qy       309 GGGCTGCTGCCCGGGGGGCACCATCTCTAACATTTTCACCTTCTGGGTTGATGGAGATAT 368
             ||| | |   ||||| ||||||  ||| ||  |  |  | ||    |     |||||| |
Db       321 GGGATCCGTTCCGGGTGGCACCTCCTCCAATGTGATTGCGTTTCTCGCCCGAGGAGATGT 380

Qy       369 GGATCTCAGCATCAGTATGACAACCTGTTCCACCGTGGCCGCCCTGGGAATGATGCCACT 428
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Qy        429 CTGCAT 434
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Db        441 CCTCAT 446
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RESULT 9
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ID AAH68532 standard; DNA; 349980 BP.
XX
AC AAH68532;
XX
DT 26-SEP-2001 (first entry)
XX
DE C glutamicum coding sequence fragment SEQ ID NO: 7067.
XX
KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KW organic acid synthesis; ds.

Corynebacterium glutamicum.

PN EP1108790-A2.
XX
PD 20-JUN-2001.
XX
PF 18-DEC-2000; 2000EP-0127688.
XX
PR 16-DEC-1999; 99JP-0377484.
PR 07-APR-2000; 2000JP-0159162.
PR 03-AUG-2000; 2000JP-0280988.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
DR WPI; 2001-376931/40.
XX
PT Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analysing
PT expression profile or pattern of a gene and identifying homologous gene
PT -
XX
PS Disclosure; SEQ ID NO: 7067; 246pp + Sequence Listing; English.
XX
CC The present invention provides a number of nucleotide and protein
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of coryneform bacterium, measuring expression amount and
CC analysing the expression profile or expression pattern of a gene derived
CC from Coryneform bacterium, and identifying a homologue of a gene derived
CC from coryneform bacterium. Coryneform bacteria are useful for producing
CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC European Patent Office.
XX
SQ Sequence 349980 BP; 80900 A; 98397 C; 92139 G; 78544 T; 0 other;

Query Match 6.0%; Score 67.6; DB 22; Length 349980;
Best Local Similarity 51.3%; Pred. No. 6.4e-09;
Matches 157; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

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Qy        189 GAGACCCTGGGGCATTGCTGTGGGACTGCTCTGCCAGTTTGGGCTCATGCCTTTTACAGC 248
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Qy        249 TTATCTCCTGGCCATTAGCTTTTCTCTGAAGCCAGTCCAAGCTATTGCTGTTCTCATCAT 308
                | | || |  |  ||     || || ||||  |  ||  |||   |||||||  |
Db      66749 GATCGTGGTTGCGAAAATGTTCAACCTCAACCCAGCACTCGCCGTTGGCCTTCTCATGCT 66690

Qy        309 GGGCTGCTGCCCGGGGGGCACCATCTCTAACATTTTCACCTTCTGGGTTGATGGAGATAT 368
              ||| | |   ||||| ||||||  ||| ||  |  |  | ||    |      |||||| |
Db      66689 GGGATCCGTTCCGGGTGGCACCTCCTCCAATGTGATTGCGTTTCTCGCCCGAGGAGATGT 66630

Qy        369 GGATCTCAGCATCAGTATGACAACCTGTTCCACCGTGGCCGCCCTGGGAATGATGCCACT 428
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Qy        429 CTGCAT 434
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Db      66569 CCTCAT 66564
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ID AAC39644 standard; DNA; 1272 BP.
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AC AAC39644;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 25386.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
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PR 26-OCT-1999; 99US-0161361.
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PR 28-OCT-1999; 99US-0161992.

PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 5.7%; Score 64.4; DB 21; Length 1272;
Best Local Similarity 49.4%; Pred. No. 2.4e-09;
Matches 167; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

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Db        225 ACAGATCTCTTTACTCTAGGTCTTGGATTTCTTATGCTTTCCATGGGTTTGACTCTTACG 284

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Qy        343 TTCACCTTCTGGGTTGATGGAGATATGGATCTCAGCATCAGTATGACAACCTGTTCCACC 402
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RESULT 11
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AC AAC49339;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 60786.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
EP1033405-A2.

06-SEP-2000.
XX
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PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 5.7%; Score 64.4; DB 21; Length 1619;
Best Local Similarity 49.4%; Pred. No. 2.7e-09;
Matches 167; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

```
Qy        103 ACAGTGGTGTCCACTGTGATGATGGGGCTGCTCATGTTCTCTTTGGGATGTTCCGTGGAG 162
              ||||   | |  ||| |     | ||  | || ||| | ||  |||| |   |  |   |
Db        382 ACAGATCTCTTTACTCTAGGTCTTGGATTTCTTATGCTTTCCATGGGTTTGACTCTTACG 441

Qy        163 ATCCGGAAGCTGTGGTCGCACATCAGGAGACCCTGGGGCATTGCTGTGGGACTGCTCTGC 222
              |      |  |  |          |  |  || |||    | | ||| ||  | ||
Db        442 TTTGAAGATTTCAGAAGATGTTTACGTAATCCATGGACGGTGGGTGTTGGTTTTCTTGCT 501

Qy        223 CAGTTTGGGCTCATGCCTTTTACAGCTTATCTCCTGGCCATTAGCTTTTCTCTGAAGCCA 282
              || | |  | ||| |||  ||  || || |||| | || || |   ||   ||   | ||
Db        502 CAATATATGATCAAGCCAATTCTAGGTTTTCTCATTGCAATGACTCTTAAGCTTTCGGCA 561

Qy        283 GTCCAAGCTATTGCTGTTCTCATCATGGGCTGCTGCCCGGGGGGCACCATCTCTAACATT 342
                | || | ||   || || |  |    |||||||| || ||       || ||| ||
Db        562 CCTCTTGCGACTGGCCTTATCCTAGTCTCATGCTGCCCTGGAGGACAGGCGTCAAACGTT 621

Qy        343 TTCACCTTCTGGGTTGATGGAGATATGGATCTCAGCATCAGTATGACAACCTGTTCCACC 402
              || | |       | ||  || | |  |||     |    |||||||| ||||| |||
Db        622 GCTACTTACATTTCCAAGGGGAATGTAGCGCTCTCTGTACTCATGACAACGTGTTCAACC 681

Qy        403 GTGGCCGCCCTGGGAATGATGCCACTCTGCATTTATCT 440
              | |  ||  |  |||||  || ||    | | | ||
Db        682 ATTGGGGCTATTATAATGACTCCTCTTCTTACTAAGCT 719
```

RESULT 12
ABL39796
ID ABL39796 standard; cDNA; 1431 BP.
XX
AC ABL39796;
XX
DT 10-MAY-2002 (first entry)
XX
DE Human NS cDNA sequence SEQ ID NO:106.
XX
KW Human; cytostatic; osteopathic; gynaecological; neuroprotective;
KW antirheumatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;
KW vasotropic; antiarteriosclerotic; antiinflammatory; dermatological;
KW anorectic; muscular; antiinfertility; cardiovascular; anticoagulant;
KW antifibrinolytic; hypotension; antiasthmatic; immunomodulator; cardiant;
KW anticonvulsant; antidiabetic; tranquilliser; antidepressant; aeuroleptic;
KW gastrointestinal; virucide; antiulcer; cerebroprotective; nootropic;
KW contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia;
KW endometriosis; degenerative disease; multiple sclerosis; psoriasis;
KW rheumatoid arthritis; cataract; restenosis; atherosclerosis; glaucoma;
KW inflammation; skin disorder; obesity; muscular dystrophy; AIDS;
KW infertility; cardiovascular disease; coagulation disease; hypertension;
KW ischaemia; asthma; immune disease; epilepsy; angina; neurodegeneration;
KW diabetes; anxiety; depression; schizophrenia; viral disease; stroke;
KW gastric ulcer; Alzheimer's disease; gene; ss.
XX
OS Homo sapiens.
XX

PN WO200206315-A2.
XX
PD 24-JAN-2002.
XX
PF 17-JUL-2001; 2001WO-IL00653.
XX
PR 18-JUL-2000; 2000IL-0137345.
PR 15-DEC-2000; 2000IL-0140354.
XX
PA (COMP-) COMPUGEN LTD.
XX
PI Mintz L, Freilich S, Bernstein J;
XX
DR WPI; 2002-155037/20.
DR P-PSDB; ABB06142.
XX
PT One hundred and twenty eight novel nucleic acid sequences, useful for
PT treating and diagnosing e.g. cancer, asthma and Alzheimer's -
XX
PS Claim 1; Page 137; 290pp; English.

CC ABL39691 to ABL39818 represent novel human nucleic acid sequences
CC encoding the proteins given in ABB06037 to ABB06164. The novel sequences
CC (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective,
CC antirheumatic, antiarthritic, antipsoriatic, ophthalmological, virucide,
CC vasotropic, antiarteriosclerotic, antiinflammatory, dermatological,
CC anorectic, muscular, anti-HIV, antiinfertility, cardiovascular,
CC anticoagulant, antifibrinolytic, hypotension, antiasthmatic, cardiant,
CC immunomodulator, anticonvulsant, antidiabetic, tranquilliser, antiulcer,
CC antidepressant, gastrointestinal, aeuroleptic, cerebroprotective,
CC nootropic and contraceptive activities. The NS can be used in vaccines,
CC gene therapy and antisense therapy. Nucleic acids, expression vectors and
CC antibodies from the present invention can be used for treating and
CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative
CC diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis,
CC cataracts, restenosis, atherosclerosis, inflammation, skin disorders,
CC glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular
CC disease, coagulation disease, ischaemia, hypertension, asthma, immune
CC disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,
CC depression, schizophrenia, viral disease, gastric ulcers, stroke,
CC Alzheimer's disease and as a contraceptive.
XX
SQ Sequence 1431 BP; 399 A; 301 C; 287 G; 421 T; 23 other;

Query Match 5.7%; Score 64.2; DB 24; Length 1431;
Best Local Similarity 46.4%; Pred. No. 2.9e-09;
Matches 283; Conservative 7; Mismatches 310; Indels 10; Gaps 3;

```
          355 GTTGATGGAGATATGGATCTCAGCATCAGTATGACAACCTGTTCCACCGTGGCCGCCCTG 414
              | ||| ||  | ||| | ||||||||||  ||||| | ||   ||||        |||||
           99 GNTGACGGCAACATGAACCTCAGCATCATCATGACCATCTCCCCCACGCNTCTGGCCCTC 158

Qy        415 GGAATGATGCCACTCTGCATTTATCTCTACACCTGGTCCTGGAGTCTTCAGCAGAATCTC 474
              |   ||||||| || ||| | |   ||||| ||| | |||| ||: || |   |||
Db        159 GTCTTGATGCCCCTGTGCCTGTGGATCTACAGCTGKGCTTGGA-TCWACACCCCTATCGT 217

Qy        475 ACCATTCCTTATCA----GAACATAGGAATTACCCTTGTGTGCCTGACCATTCCTGTGGC 530
                |  || ||    |      || | |      | || ||      |:     ||| ||| | |
Db        218 GCAGTTACTACCCCTAGGGACCGTGACCCTNACTCTCTGCAGMACTCTCATACCTATCGG 277

Qy        531 CTTTGGTGTCTATGTGAATTACAGATGGCCAAAACAATCCAAAATCATTCTCAAGAT--- 587
              || || |||:   |    ||| |          | ||   |||| | ||| |
Db        278 GTTGGGCGTCYTCATTCGCNACAAAAACAGCCGGGTGGCTAACTACATTGTGAAGGTTTC 337

Qy        588 --TGGGGCCGTTGTTGGTGGGGTCCTCCTTCTGGTGGTCGCAGTTGCTGGTGTGGTCCTG 645
                || || |  || | ||          ||   |      |          ||   |
Db        338 CCTGTGGTCTCTGCTAGTAACTCTGGTGGTCCTTTTCATAATGACCGGCACTATGTTAGG 397

Qy        646 GCGAAAGGATCTTGGAATTCAGACATCACCCTTCTGACCATCAGTTTCATCTTTCCTTTG 705
              |   |    || | || |    |  || |  | |        ||     | | | | ||
Db        398 ACCTGAACGGCTGGCAAGTATCCCYGCAGCTGTTTATGTGATAGCAATTTTTATGCCTTT 457

Qy        706 ATTGGCCATGTCACGGGTTTTCTGCTGGCACTTTTTACCCACCAGTCTTGGCAAAGGTGC 765
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              |  | |   | |||| |    | ||   | |   ||: |   |    ||  |
Db        458 GGCAGNTACGCTTCAGGTTATGGTTTAGCCACTCTCTTCCMTCTTCCACCCCACTGCAAG 517

Qy        766 AGGACAATTTCCTTAGAAACTGGAGCTCAGAATATTCAGATGTGCATCACCATGCTCCAG 825
              |||||  | |   | ||||| ||   ||||||| | ||| | ||:|   |||| ||  :
Db        518 AGGACTGTATGTCTGGAAACAGGTAGTCAGAATGTGCAGCTCTGSACAGCCATTCTAAMA 577

Qy        826 TTATCTTTCACTGCTGAGCACTTGGTCCAGATGTTGAGTTTCCCACTGGCCTATGGACTC 885
              |  | ||  |  |  |    | | |      |||   |  || ||  ||   |||| |||
Db        578 CTGGCCTTTCCACCGCAATTCATAGGAAGCATGGACATGTTTCCTTTGCTGTATGCACTT 637

Qy        886 TTCCAGCTGATAGATGGATTTCTTATTGTTGCAGCATATCAGACGTACAAGAGGAGATTG 945
              ||||||     ||| |       || |||||  |   ||| | | |||   ||   | ||
Db        638 TTCCAGTCTGCAGAAGCGGGGATTTTTGTTTTAATCTATAAAATGTATGGAAGTGAAATG 697

Qy        946 AAGAACAAAC 955
                | |||| |
Db        698 TKGCACAAGC 707
```

RESULT 13
AAF28554/c
ID AAF28554 standard; DNA; 269223 BP..
XX
AC AAF28554;
XX
DT 04-APR-2001 (first entry)
XX
DE Genomic fragment #41.
XX
KW Genomic library; bacteria; human upper airway; otitis media; sinusitis;
KW bronchopulmonary; endocarditis; meningitis; ss.
XX
OS Moraxella catarrhalis.
XX
PN WO200078968-A2.
XX
PD 28-DEC-2000.
XX
PF 16-JUN-2000; 2000WO-US16649.
XX
PR 18-JUN-1999; 99US-0140121.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lagace RE, Patterson C, Berg KL;
XX
DR WPI; 2001-041427/05.
XX
PT Genomic library for identifying diagnostic and therapeutic
PT compositions, and for identifying virulence factors, regulatory
PT elements and drug targets, comprises Moraxella catarrhalis nucleic
PT acids -
XX
PS Claim 1; Page 486-545; 545pp; English.
XX
CC The present invention relates to a Moraxella catarrhalis genomic library
CC comprising of a combination of 41 nucleic acid molecules (see
CC AAF28514-AAF28554). The library has a number of uses described in the
CC specification e.g. is useful for aidentifying diagnostic and therapeutic
CC compositions. M. catarrhalis (Branhamella catarrhalis) is a large
CC aerobic, gram-negative diplococcus, normally found among the bacterial
CC flora of human upper airways. M. catarrhalis is known to cause acute,
CC localised infections such as otitis media, sinusitis and bronchopulmonary
CC infection and life-threatening, systemic diseases including endocarditis
CC and meningitis.
XX
SQ Sequence 269223 BP; 77067 A; 56596 C; 57380 G; 78180 T; 0 other;

Query Match 5.1%; Score 58.2; DB 22; Length 269223;
Best Local Similarity 48.4%; Pred. No. 5.1e-06;
Matches 162; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

```
Qy        122 TGATGGGGCTGCTCATGTTCTCTTTGGGATGTTCCGTGGAGATCCGGAAGCTGTGGTCGC 181
              || | |  |  |||||| |     |||| |   || ||    ||    |  | |
Db     183238 TGCTTGGCATCGTCATGCTTGGCATGGGTTTAACCTTGACTTTCAAAGATTTTGGTGAAG 183179

Qy        182 ACATCAGGAGACCCTGGGGCATTGCTGTGGGACTGCTCTGCCAGTTTGGGCTCATGCCTT 241
              || ||  |  |||  ||   |   | | ||  |  ||   || | ||   | |||||
Db     183178 TCACCAAAAACCCCAAGGCGGTGATTATTGGCGTTATCCTTCAATATGTTGTGATGCCAG 183119

Qy        242 TTACAGCTTATCTCCTGGCCATTAGCTTTTCTCTGAAGCCAGTCCAAGCTATTGCTGTTC 301
              | |  || | | |  |||       |||   ||    || |     ||||| | |||
Db     183118 TCATTGCCTTTTTGTTGGTTCAAGCATTTAGGCTACCACCTGATTTGGCTATCGGTGTCA 183059

Qy        302 TCATCATGGGCTGCTGCCCGGGGGGCACCATCTCTAACATTTTCACCTTCTGGGTTGATG 361
              || |  | ||||||||||| || ||||||   || ||  |  |||| ||    |   | |
Db     183058 TCTTAGTCGGCTGCTGCCCTGGCGGCACCTCGTCAAATGTCATCACTTTTCTTGCCAAAG 182999

Qy        362 GAGATATGGATCTCAGCATCAGTATGACAACCTGTTCCACCGTGGCCGCCCTGGGAATGA 421
              |  |||  | | |      |   |   || ||    |||||  |    ||||      |||
Db     182998 GCAATACCGCTTTATCAGTTGCTTGCACGACACTCTCCACACTCTTAGCCCCTATTTTGA 182939

Qy        422 TGCCACTCTGCATTTATCTCTACACCTGGTCCTGG 456
              ||||       ||||| | |   || |    |||
Db     182938 CGCCAGCTGTATTTTATTTATTTGCCAGCCAATGG 182904
```

RESULT 14
AAD22002
ID AAD22002 standard; cDNA; 2141 BP.
XX
AC AAD22002;
XX
DT 12-FEB-2002 (first entry)
XX
DE Human transporters and ion channels (TRICH)-10 cDNA.
XX
KW Human; transporter and ion channel; TRICH; akinesia; cystic fibrosis;
KW diabetes mellitus; Parkinson's disease; myasthenia gravis; dementia;
KW cardiac disorder; angina; hypertension; myocarditis; hyperglycaemia;
KW neurological disorder; Alzheimer's disease; cataract; infertility;
KW Wilson's disease; schizophrenia; Grave's disease; addison's disease;
KW Huntington's disease; multiple sclerosis; meningitis; hypotensive;
KW cardiant; nootropic; neuroprotective; neuroleptic; ophthalmological;
KW antithyroid; anticonvulsant; goitre; antiinflammatory; ss.
XX
OS Homo sapiens.
XX

Key	Location/Qualifiers
CDS	69..1544
	/*tag= a
FT	/product= "Human transporters and ion channels
FT	(TRICH)-10"

XX
PN WO200177174-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-US11206.
XX
PR 06-APR-2000; 2000US-195595P.
PR 12-APR-2000; 2000US-196872P.
PR 20-APR-2000; 2000US-199020P.
PR 28-APR-2000; 2000US-200552P.
PR 05-MAY-2000; 2000US-202348P.
PR 11-MAY-2000; 2000US-203495P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Reddy R, Thornton M, Borowsky ML, Tang YT, Khan FA, Tribouley CM;
PI Gandhi AR, Yao MG, Sanjanwala MS, Baughn MR, Nguyen DB;
PI Policky JL, Yue H, Seilhamer JJ, Walia NK, Lal P, Kearney L;
PI Walsh RT, Lu DAM, Lu Y, Greene BD, Raumann BE, Patterson C;
XX
DR WPI; 2002-017448/02.
DR P-PSDB; AAE13283.
XX
PT Polypeptides of human transporters and ion channels, useful for
PT diagnosing, treating or preventing disorders of transport,
PT neurological, muscle, immunological and cell proliferative disorders -
XX
PS Claim 5; Page 145-146; 150pp; English.
XX
CC The invention relates to human transporters and ion channels (TRICH)
CC and the polynucleotides encoding them. The composition comprising TRICH
CC or agonist of TRICH is useful for treating a disease or condition
CC associated with decreased expression of functional TRICH or condition
CC associated with overexpression of TRICH respectively. The composition
CC comprising Ab is useful for diagnosing a condition of disease associated
CC with expression of TRICH in a subject, where the disorders include a
CC transport disorder such as akinesia, cystic fibrosis, diabetes mellitus,
CC Parkinson's disease, myasthenia gravis, cardiac disorders associated
CC with transport e.g. angina, hypertension, myocarditis, neurological
CC disorders associated with transport e.g. Alzheimer's disease, Wilson's
CC disease, schizophrenia, cataracts, infertility, hyperglycaemia, Grave's
CC disease, goitre, addison's disease, Huntington's disease, dementia,
CC multiple sclerosis, bacterial and viral meningitis. TRICH DNA is useful
CC for generating a transcript image of a tissue or cell type, which
CC represents the global pattern of gene expression by a particular tissue
CC or cell type and for analysing the proteome of a tissue or cell type.
CC TRICH DNA is used in gene therapy. The present sequence is human
CC TRICH10 cDNA.
XX
SQ Sequence 2141 BP; 505 A; 573 C; 505 G; 558 T; 0 other;

Query Match 5.1%; Score 57.6; DB 24; Length 2141;
Best Local Similarity 48.5%; Pred. No. 4.5e-07;
Matches 288; Conservative 0; Mismatches 289; Indels 17; Gaps 4;

```
Qy        375 CAGCATCAGTATGACAACCTGTTCCACCGTGGCCGCCCTGGGAATGATGCCACTCTGCAT 434
              ||||||||  ||||| | ||  |||||  |    ||||| |   ||||||| || ||| |
Db        818 CAGCATCATCATGACCATCTCCTCCACGCTTCTGGCCCTCGTCTTGATGCCCCTGTGCCT 877

Qy        435 TTATCTCTACACCTGGTCCTGGAGTCTTCAGCAGAATCTCACCATTCCTTATCA----GA 490
              |  |||||| |||| | |||| ||  || |   |||   |  || ||   |     ||
Db        878 GTGGATCTACAGCTGGGCTTGGA-TCAACACCCCTATCGTGCAGTTACTACCCCTAGGGA 936

Qy        491 ACATAGGAATTACCCTTGTGTGCCTGACCATTCCTGTGGCCTTTGGTGTCTATGTGAATT 550
              | |     | || ||      ||     ||| ||| | |  || || |||   |    |
Db        937 CCGTGACCCTGACTCTCTGCAGCACTCTCATACCTATCGGGTTGGGCGTCTTCATTCGCT 996

Qy        551 ACAGATGGCCAAAACAATCCAAAATCATTCTCAAGATTGGGGCCGTTGTTGGTGGGGTCC 610
              |||  ||          |  |   |||| | ||| ||    ||  |      |  | |
Db        997 ACAAATACAGCCGGGTGGCTGACTACATTGTGAAGGTTT---CCCTGTGGTCTCTGCTAG 1053

Qy        611 TCCTTCTGGTGGTCGCAGTTGCTGGTGTGGTCCTGGCGAAAGGATCTTGGAATTCAGACA 670
              |  ||||||||||    |          | |      |  |||| ||        |  |
Db       1054 TGACTCTGGTGGTCCTTTTCATAATGACCGGCACTATGTTAGGACCTGAACTGCTGGCAA 1113

Qy        671 TCACCCTTCTGACCATCAGTTTCA---------TCTTTCCTTTGATTGGCCATGTCACGG 721
              | || |    |  |   | | |          |  | ||||||   ||| | |   | |
Db       1114 GTATCCCTGCAGCTGTTTATGTGATAGCAATTTTTATGCCTTTGGCAGGCTACGCTTCAG 1173

Qy        722 GTTTTCTGCTGGCACTTTTTACCCACCAGTCTTGGCAAAGGTGCAGGACAATTTCCTTAG 781
              ||| |    | ||  | |   ||| |   |    |  |    |||||  | |   | |
Db       1174 GTTATGGTTTAGCTACTCTCTTCCATCTTCCACCCAACTGCAAGAGGACTGTATGTCTGG 1233

Qy        782 AAACTGGAGCTCAGAATATTCAGATGTGCATCACCATGCTCCAGTTATCTTTCACTGCTG 841
              |||| ||   |||||||  | ||| | || |   |||| ||  |  |  | ||  | |
Db       1234 AAACAGGTAGTCAGAATGTGCAGCTCTGTACAGCCATTCTAAAACTGGCCTTTCCACCGC 1293

Qy        842 AGCACTTGGTCCAGATGTTGAGTTTCCCACTGGCCTATGGACTCTTCCAGCTGATAGATG 901
              |   | | |     ||||  |  || ||  ||    |||| ||| ||||||     ||| |
Db       1294 AATTCATAGGAAGCATGTACATGTTTCCTTTGCTGTATGCACTTTTCCAGTCTGCAGAAG 1353

Qy        902 GATTTCTTATTGTTGCAGCATATCAGACGTACAAGAGGAGATTGAAGAACAAAC 955
                  || |||||  |   ||| | | |||    ||   | ||  | |||| |
Db       1354 CGGGGATTTTTGTTTTAATCTATAAAATGTATGGAAGTGAAATGTTGCACAAGC 1407
```

```
RESULT 15
AAH66357
ID   AAH66357 standard; DNA; 1005 BP.
XX
AC   AAH66357;
XX
DT   26-SEP-2001  (first entry)
XX
DE   C glutamicum coding sequence fragment SEQ ID NO: 1392.
XX
KW   Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KW   organic acid synthesis; ds.
XX
OS   Corynebacterium glutamicum.
XX
PN   EP1108790-A2.
XX
PD   20-JUN-2001.
XX
PF   18-DEC-2000; 2000EP-0127688.
XX
PR   16-DEC-1999;   99JP-0377484.
PR   07-APR-2000; 2000JP-0159162.
PR   03-AUG-2000; 2000JP-0280988.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Nakagawa S,  Mizoguchi H,  Ando S,  Hayashi M,  Ochiai K,  Yokoi H;
PI   Tateishi N,  Senoh A,  Ikeda M,  Ozaki A;
XX
DR   WPI; 2001-376931/40.
DR   P-PSDB; AAG91138.
XX
PT   Novel polynucleotides derived from Coryneform bacteria, for identifying
PT   mutation point of a gene, measuring expression of a gene, analysing
PT   expression profile or pattern of a gene and identifying homologous gene
PT   -
XX
PS   Claim 8; SEQ ID NO: 1392; 246pp + Sequence Listing; English.
XX
CC   The present invention provides a number of nucleotide and protein
CC   sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC   are useful for identifying the mutation point of a gene derived from a
CC   mutant of coryneform bacterium, measuring expression amount and
CC   analysing the expression profile or expression pattern of a gene derived
CC   from Coryneform bacterium, and identifying a homologue of a gene derived
CC   from coryneform bacterium. Coryneform bacteria are useful for producing
CC   amino acids, nucleic acids, vitamins, saccharides and organic acids,
CC   particularly L-lysine. The present sequence is a nucleic acid described
CC   in the exemplification of the invention.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from the
CC   European Patent Office.
XX
SQ   Sequence 1005 BP; 179 A; 284 C; 261 G; 281 T; 0 other;

  Query Match             4.7%;  Score 53.6;  DB 22;  Length 1005;
  Best Local Similarity   47.4%;  Pred. No. 5.3e-06;
  Matches  161;  Conservative    0;  Mismatches  179;  Indels    0;  Gaps    0;

Qy         89 TGGAGCTCGTTTTCACAGTGGTGTCCACTGTGATGATGGGGCTGCTCATGTTCTCTTTGG 148
              | | ||||  | |  |   |  |  || |    || ||||  |  ||||||||||  |||
Db        122 TTGTGCTCAATATTTCTTCGTGGGTCAATCCTTTGCTGGGCATCATCATGTTCTCCATGG 181

Qy        149 GATGTTCCGTGGAGATCCGGAAGCTGTGGTCGCACATCAGGAGACCCTGGGGCATTGCTG 208
              |    || || ||    |  |           |   | ||       ||  |
Db        182 GCCTGACCTTGAAGCCAGTTGACTTCGCCCTTGTTGCTAAACGCCCACTCCCAGTTCTTA 241

Qy        209 TGGGACTGCTCTGCCAGTTTGGGCTCATGCCTTTTACAGCTTATCTCCTGGCCATTAGCT 268
              | ||  || ||  ||||||||  |||||||  | |  || |  ||  ||| |       |
Db        242 TCGGCGTGATCGCCCAGTTTGTCATCATGCCCCTGATCGCATTGCTGGTGGTCTGGGTTT 301

Qy        269 TTTCTCTGAAGCCAGTCCAAGCTATTGCTGTTCTCATCATGGGCTGCTGCCCGGGGGGCA 328
              |    |||    | |    ||    | |||  || |  | || ||    || || || |
Db        302 TGCAGCTGCCTGCGGAAATTGCGGCCGGTGTCATCTTGGTTGGTTGTGCACCTGGCGGAA 361

Qy        329 CCATCTCTAACATTTTCACCTTCTGGGTTGATGGAGATATGGATCTCAGCATCAGTATGA 388
              |   ||| ||| |  | | | |  |     ||| ||| | |  ||     |||  ||||
Db        362 CTTCCTCCAACGTGGTGTCTTACCTGTCCCGTGGTGATGTTGCGCTGTCTGTCACCATGA 421

Qy        389 CAACCTGTTCCACCGTGGCCGCCCTGGGAATGATGCCACT 428
              |  ||   ||||  ||   || |     | |  ||||
Db        422 CTTCCATCTCCACGCTGCTTGCTCCAATTTTCACTCCACT 461

Search completed: June  9, 2003, 05:35:48
Job time : 305 secs
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